

Sequence Listing

<110> ASHKENAZI, AVI J
 BOTSTEIN, DAVID
 DODGE, KELLY H.
 GURNEY, AUSTIN L.
 KIM, KYUNG JIN
 LAWRENCE, DAVID A.
 PITTI, ROBERT
 ROY, MARGARET A
 TUMAS, DANIEL B
 WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

<160> 18

<210> 1

<211> 300

<212> PRT

<213> Homo sapiens

<400> 1

Met	Arg	Ala	Leu	Glu	Gly	Pro	Gly	Leu	Ser	Leu	Leu	Cys	Leu	Val
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Leu	Ala	Leu	Pro	Ala	Leu	Leu	Pro	Val	Pro	Ala	Val	Arg	Gly	Val
			20						25					30

Ala	Glu	Thr	Pro	Thr	Tyr	Pro	Trp	Arg	Asp	Ala	Glu	Thr	Gly	Glu
			35						40					45

Arg	Leu	Val	Cys	Ala	Gln	Cys	Pro	Pro	Gly	Thr	Phe	Val	Gln	Arg
			50						55					60

Pro	Cys	Arg	Arg	Asp	Ser	Pro	Thr	Thr	Cys	Gly	Pro	Cys	Pro	Pro
			65						70					75

Arg	His	Tyr	Thr	Gln	Phe	Trp	Asn	Tyr	Leu	Glu	Arg	Cys	Arg	Tyr
			80						85					90

Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys	
				95					100					105	
His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe	
				110					115					120	
Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly	
				125					130					135	
Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys	
				140					145					150	
Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser	
				155					160					165	
Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala	
				170					175					180	
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	
				185					190					195	
Cys	Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	
				200					205					210	
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	
				215					220					225	
Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu	
				230					235					240	
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu	
				245					250					255	
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly	
				260					265					270	
Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met	
				275					280					285	
Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His	
				290					295					300	

<210> 2
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1090

<223> Unknown base

<400> 2

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agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100
atgagggcgc tggagggggc aggccgtgctg ctgctgtgcc tgggtgttggc 150
gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200
ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250
cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300
cacgacgtgt ggcccgtgtc caccgcgccca ctacacgcag ttctggaact 350
acctggagcg ctgccgtac tgcaacgtcc tctgcgggga gcgtgaggag 400
gaggcacggg cttgccacgc caccacaaac cgtgcctgcc gctgccgcac 450
cggtctcttc gcgcacgctg gtttctgctt ggagcacgca tcgtgtccac 500
ctgggtgccg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550
cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600
gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650
caggctcttc ctcccatgac accctgtgca ccagctgcac tggcttcccc 700
ctcagcacca ggggtaccagg agctgaggag tgtgagcgtg ccgtcatcga 750
ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800
aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850
gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tcctgggggc 900
gcaggacggg gcgctgctgg tgccgctgct gcaggcgtg cgcgtggcca 950
ggatgcccgg gctggagcgg agcgtccgtg agcgttcct ccctgtgcac 1000
tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050
ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaaa 1100
aaaaaaaaaa aaaa 1114

<210> 3

<211> 491

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

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cagttctgga antaactgga gcncctgccg tactgnaacg tcctctgngg 100
ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgect 150
gccgctgccg caccggcttc ttcgcgcacg ctggtttctg cttggagcac 200
gcatcgtgtc cacctgggtgc cggcgtgatt gcccgggca cccccagcca 250
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300
tccagctcag agcagtgccg gcccaccgc aactgcaagg ccctgggect 350
ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400
gcactggctt cccctcagc accagggtag caggagctga ggagtgtgag 450
cgtgccgtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 4
gccgagacag cccacgacg tgtggcccg gtccaccg ccaactacag 50
cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

<223> unknown base

<400> 5

gccgagacag ccccaacgacg tgtggcccggt gtccaccgcg cnactacacg 50

cagttctgga antaactgga gncctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccaccac aaccgcgcct 150

gncgtgcag caccggnctt ttgcgcacg ctgntttctg cttggagcac 200

gcacgtgtc cacctggtgn cggcgtgatt gncccgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6

<211> 201

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>

<221> unsure

<222> 182

<223> unknown base

<400> 6

gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg 50

gggagcgtga ggaggaggca cgggcttgcc acgccacca caaccgtgcc 100

tgccgctgcc gcaccggctt cttgcgcac gctggtttct gcttgagca 150

cgcacgtgt ccacctggtg ccggcgtgat tnccccgggc acccccagcc 200

a 201

<210> 7

<211> 277

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgc 50
ggteccagcc ttgcacctg agctaggaca ccagttcccc tgacctgtt 100
cttccctect ggctgcaggc acccccagcc agaacacgca gnccagccgt 150
gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250
ttcttcccat gacacctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca cccccagcca 50
gaacacgcag gcctagccgt gccccccagg caccttctca gccagcagct 100
ccagctcaga gcagtgccag cccccaccgca actgcacggc cctgggcctg 150
gccctcaatg tgccaggctc ttcttcccat gacacctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
agcngtgenc cncaggcacc ttctcagcca gcagttccag ctccagagcag 50

tgccagcccc accgcaactg cacggccctg ggccctggccc tcaatgtgcc 100
 aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttccccc 150
 tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200
 tttgtggctt tccaggacat ctccat 226

<210> 10
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Unsure
 <222> 1-283
 <223> Unknown organism

<220>
 <221> unsure
 <222> 27, 64, 140
 <223> unknown base

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 cgcagtgcc a gcentccccc caggcacctt ctcagccagc agctccagct 100
 cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150
 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200
 ttccccctca gcaccagggg accaggagct gaggagtgtg agcgtgccgt 250
 catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
 <211> 21
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown organism

<400> 11
 cacgctgggt tctgcttgga g 21

<210> 12
 <211> 22
 <212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 12

agctggtgca caggggtgtca tg 22

<210> 13

<211> 53

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 13

cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 14

acacgatgcg tgctccaagc agaa 24

<210> 15

<211> 17

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 15

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<210> 16

<211> 16

<212> DNA

<213> Unknown

<220>

<223> Unknown organism

<400> 16
atcacgccgg caccag 16

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17
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Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr
20 25 30
Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
35 40 45
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
50 55 60
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
65 70 75
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
80 85 90
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
95 100 105
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
110 115 120
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
125 130 135
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
140 145 150
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
155 160 165
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
170 175 180
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
185 190 195
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
200 205 210

Pro Gly Ala Val	His Leu Pro Gln Pro	Val Ser Thr Arg Ser Gln	215	220	225
His Thr Gln Pro	Thr Pro Glu Pro Ser	Thr Ala Pro Ser Thr Ser	230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro	Pro Ala Glu Gly Ser Thr	245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu	Ile Val Gly Val Thr Ala	260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val	Asn Cys Val Ile Met Thr	275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu	Gln Arg Glu Ala Lys Val	290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg	Gly Thr Gln Gly Pro Glu	305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro	Ser Ser Ser Ser Ser Ser	320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp	Arg Arg Ala Pro Thr Arg	335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu	Ala Ser Gly Ala Gly Glu	350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp	Ser Ser Pro Gly Gly His	365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile	Val Asn Val Cys Ser Ser	380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser	Gln Ala Ser Ser Thr Met	395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu	Ser Pro Lys Asp Glu Gln	410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala	Phe Arg Ser Gln Leu Glu	425	430	435
Thr Pro Glu Thr	Leu Leu Gly Ser Thr	Glu Glu Lys Pro Leu Pro	440	445	450
Leu Gly Val Pro	Asp Ala Gly Met Lys	Pro Ser	455	460	

[illegible]

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
1 5 10 15

Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
35 40 45

Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
65 70 75

Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
95 100 105

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
125 130 135

Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
155 160 165

His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
185 190 195

Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
215 220 225

Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
				230					235					240	
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	
				245					250					255	
Leu	Trp	Lys	His	Gln	Asn	Lys	Ala	Gln	Asp	Ile	Val	Lys	Lys	Ile	
				260					265					270	
Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	
				275					280					285	
Gly	His	Ala	Asn	Leu	Thr	Phe	Glu								
				290											